

Aberystwyth University

The complete mitochondrial genome of record-breaking migrant Arctic tern (Sterna paradisaea)

Skujina, Ilze; Healey, Amy; de Becquevort, Sophie Marie Catherine; Shaw, Paul; McMahon, Robert; Morgan, Charly; Evans, Caron; Taylor, Rachel; Hegarty, Matthew; McKeown, Niall

Published in:
Mitochondrial DNA Part B

DOI:
[10.1080/23802359.2019.1644225](https://doi.org/10.1080/23802359.2019.1644225)

Publication date:
2019

Citation for published version (APA):
Skujina, I., Healey, A., de Becquevort, S. M. C., Shaw, P., McMahon, R., Morgan, C., Evans, C., Taylor, R., Hegarty, M., & McKeown, N. (2019). The complete mitochondrial genome of record-breaking migrant Arctic tern (*Sterna paradisaea*). *Mitochondrial DNA Part B*, 4(2), 2738-2739.
<https://doi.org/10.1080/23802359.2019.1644225>

Document License CC BY

General rights

Copyright and moral rights for the publications made accessible in the Aberystwyth Research Portal (the Institutional Repository) are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the Aberystwyth Research Portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the Aberystwyth Research Portal

Take down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

tel: +44 1970 62 2400
email: is@aber.ac.uk



Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

The complete mitochondrial genome of record-breaking migrant Arctic tern (*Sterna paradisaea*)

Ilze Skujina, Amy Jane Elizabeth Healey, Sophie de Becquevort, Paul William Shaw, Robert McMahon, Charly Morgan, Caron Evans, Rachel Taylor, Matthew Hegarty & Niall Joseph McKeown

To cite this article: Ilze Skujina, Amy Jane Elizabeth Healey, Sophie de Becquevort, Paul William Shaw, Robert McMahon, Charly Morgan, Caron Evans, Rachel Taylor, Matthew Hegarty & Niall Joseph McKeown (2019) The complete mitochondrial genome of record-breaking migrant Arctic tern (*Sterna paradisaea*), Mitochondrial DNA Part B, 4:2, 2738-2739, DOI: [10.1080/23802359.2019.1644225](https://doi.org/10.1080/23802359.2019.1644225)

To link to this article: <https://doi.org/10.1080/23802359.2019.1644225>



© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 22 Jul 2019.



Submit your article to this journal [↗](#)



Article views: 79





View Crossmark data [↗](#)

MITOGENOME ANNOUNCEMENT



The complete mitochondrial genome of record-breaking migrant Arctic tern (*Sterna paradisaea*)

Ilze Skujina^a , Amy Jane Elizabeth Healey^a , Sophie de Becquevort^a, Paul William Shaw^a, Robert McMahon^b, Charly Morgan^a, Caron Evans^a, Rachel Taylor^c, Matthew Hegarty^a and Niall Joseph McKeown^a

^aInstitute of Biology, Environmental and Rural Sciences at Aberystwyth University, Aberystwyth, Wales, UK; ^bDepartment of Molecular Haematology, Haematology Laboratory, Royal Infirmary of Edinburgh, Edinburgh, Scotland, UK; ^cBritish Trust for Ornithology, Thetford, UK

ABSTRACT

The analysis of mitochondrial DNA (mtDNA) base composition, codon usage, and genome arrangement patterns can provide insight into metabolic pathways and evolutionary history. Here, we report on the complete mitochondrial genome (mitogenome) of Arctic tern (*Sterna paradisaea*) a species notable for undertaking the longest migrations of any species as well as breeding in sub-polar habitats and capable of enduring extreme altitude. The complete mitogenome was 16,708 bp long and was typical of other avian mitogenomes in size and content. The phylogenetic position of the Arctic tern within Charadriiformes based on the coding region on the mtDNA corresponded closely to that based on nuclear loci. The sequence will provide a useful resource for investigations of metabolic adaptations of this remarkable species.

ARTICLE HISTORY

Received 20 June 2019
Accepted 10 July 2019

KEYWORDS



Sterna paradisaea; mtDNA; complete mitogenome; long-lived migrant

The terns (*Charadriiformes: Laridae: Sternini*) are cosmopolitan core water birds closely related to the gulls, noddies, and skimmers. The life histories of 12 generally accepted genera of terns range from that of entirely sedentary to strongly migratory species (Cramp 1985). Among these, the Arctic tern (*Sterna paradisaea*) holds the record for the longest roundtrip animal migration ever recorded electronically (Egevang et al. 2010). Arctic terns also reach long-lifespans despite life-long high energy expenditures and exposure to hypoxia associated with extreme conditions such as cold and high altitude flight (Hatch 1974). We used Illumina MiSeq platform to sequence the whole genome from heart tissue of a casualty Arctic tern (N53.42129° W4.60853°) – kindly donated by British Trust for Ornithology (available at IBERIS Natural History Museum Tissue Collection: accession AT001). Shotgun libraries were prepared using the Nextera XT DNA Sample Preparation Kit (Illumina, San Diego, USA) of Qiagen DNeasy (Qiagen Ltd, West Sussex, UK) extracted DNA from mitochondrial-enriched DNA fraction obtained by differential centrifugation. The Illumina MiSeq run generated 8,468,804 paired-end reads that were mapped to complete *Sterna hirundo* genome (NCBI GenBank: MF582632; Yang et al. 2017) used as a reference on CLC Genomic Workbench v3.6 (CLC Bio, Aarhus, Denmark). In total, 1.09% of the raw reads mapped to the *Sterna hirundo* mtDNA and yielded two ~12kb and ~3kb contigs that covered 95.62% of the reference genome. Sanger sequencing was used, to add the

missing control region (CR) sequence (1158 bp) and to confirm that no CR duplications (Skujina et al. 2017) was present in this species. The complete mitogenome sequence of the Arctic tern (GenBank: MK946458) was 16,708 bp with heavy strand GC composition of 44.10% and encoded the 37 vertebrate mtDNA genes in the order that is considered standard for the Aves (Gibb et al. 2007).

For 10 out of the 13 mitochondrial protein coding genes (PCG) of *Sterna paradisaea*, the traditional AUG codon was used for initiation (Drabkin and Rajbhandary 1998), whereas COX1 and ND5 genes were initiated by GUG and ND3 by AUC. Traditional mitochondrial open reading frame stop codons of AGG, AGA, UAA, or UAG was used for all genes apart from COX3, ND2, and ND4 which had incomplete stop codon (T) that is completed by the addition of 3' A residues to the mRNA. The ND3 gene had a nucleotide base C in 9693 site that is not translated, although the frameshift mechanism is unknown (Mindell et al. 1998).

Phylogenetic position of the newly assembled complete Arctic tern mitogenome coding sequence within the Charadriiformes was resolved in MEGA 7 (Kumar et al. 2016) by maximum likelihood (ML) tree (Figure 1) following the method of Tamura and Nei (1993). Phylogenetic relationships aligned with those reported by Prum et al. (2015) based on 259 nuclear loci including 390,000 bp of 198 species of extant birds. Given its central role in energy metabolism, comparison of the mitochondrial DNA (mtDNA) of closely related

CONTACT Ilze Skujina  ilze.skujina@gmail.com  Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Edward Llwyd Building, Z1.03 Penglais, Ceredigion, Aberystwyth, SY23 3DA, UK

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

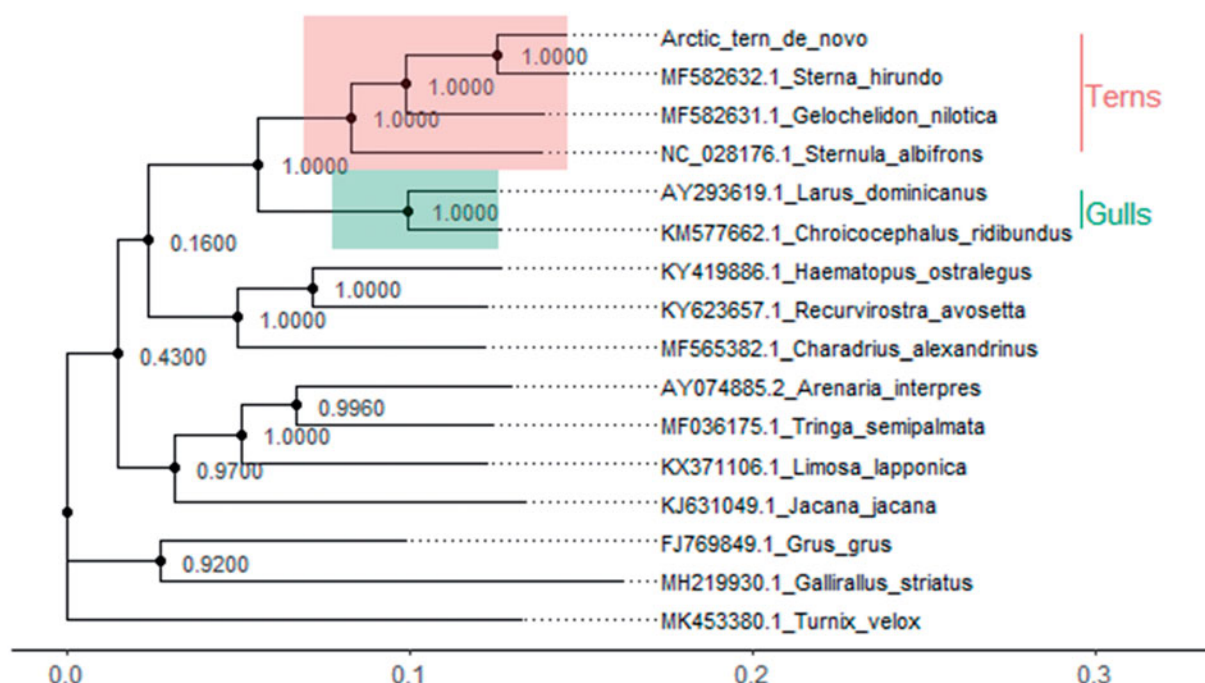


Figure 1. ML inferred phylogenetic relationships among *Charadriiformes* based on available mitochondrial coding region nucleotide sequences that corresponded to high resolution avian nuclear phylogenetic tree as constructed by (Prum et al. 2015). Annotation was created in R using 'ggtree' package (Yu et al. 2017, 2018).

species with different life-histories should provide a better understanding of the adaptive response to environmental stress.

Acknowledgements

We thank *British Trust for Ornithology* for kindly donating the specimen. This research was generously supported by the *Dr Owen Price PhD scholarship*.

Disclosure statement

No potential conflict of interest was reported by the authors.

ORCID

Ilze Skujina  <http://orcid.org/0000-0002-0329-8047>

Amy Jane Elizabeth Healey  <http://orcid.org/0000-0001-6061-0044>

References

- Cramp S. 1985. The Birds of the Western Palearctic. Vol. 4. Oxford (UK): Oxford University Press.
- Drabkin HJ, RajBhandary UL. 1998. Initiation of protein synthesis in mammalian cells with codons other than AUG and amino acids other than methionine. *Mol Cell Biol.* 18:5140–5147.
- Egevang C, Stenhouse IJ, Phillips RA, Petersen A, Fox JW, Silk JR. 2010. Tracking of Arctic terns *Sterna paradisaea* reveals longest animal migration. *Proc Natl Acad Sci USA.* 107:2078–2081.
- Gibb GC, Kardailsky O, Kimball RT, Braun EL, Penny D. 2007. Mitochondrial genomes and avian phylogeny: complex characters and resolvability without explosive radiations. *Mol Cell Biol.* 24: 269–280.
- Hatch JJ. 1974. Longevity record for the Arctic tern. *Bird-Banding.* 45: 269–270.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Cell Biol.* 33: 1870–1874.
- Mindell DP, Sorenson MD, Dimcheff DE. 1998. An extra nucleotide is not translated in mitochondrial ND3 of some birds and turtles. *Mol Biol Evol.* 15:1568–1571.
- Prum RO, Berv JS, Dornburg A, Field DJ, Townsend JP, Lemmon EM, Lemmon AR. 2015. A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. *Nature.* 526:569.
- Skujina I, McMahon R, Hegarty M. 2017. Re-interpreting mitogenomes: are nuclear/mitochondrial sequence duplications correctly characterised in published sequence databases? *Insights Genet Genom.* 1: 6–1.
- Tamura K, Nei M. 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Mol Biol Evol.* 10:512–526.
- Yang C, Wang QX, Li XJ, Yuan H, Xiao H, Huang Y. 2017. The mitogenomes of *Gelochelidon nilotica* and *Sterna hirundo* (*Charadriiformes, Sternidae*) and their phylogenetic implications. *Mitochondr DNA B Resour.* 2:601–603.
- Yu G, Lam TT, Zhu H, Guan Y. 2018. Two methods for mapping and visualizing associated data on phylogeny using ggtree. *Mol Biol Evol.* 35: 3041–3043.
- Yu G, Smith D, Zhu H, Guan Y, Lam TT. 2017. *ggtree*: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods Ecol Evol.* 8:28–36.